

SEQUENCE LISTING

<110> CINES, Douglas B
HIGAZI, Abd Al-Roof

<120> COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TISSUE CONTRACTABILITY

<130> 9596-331

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<150> US 60/212,847

<151> 2000-06-20

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 88

<212> PRT

<213> Homo sapiens

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Leu	Gln	Gln	Thr	Tyr	His	Ala	His	Arg	Ser	Asp	Ala	Leu	Gln	Leu	Gly
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Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Asn	Arg	Arg	Arg	Pro
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Trp	Cys	Tyr	Val	Gln	Val	Gly	Leu	Lys	Pro	Leu	Val	Gln	Glu	Cys	Met
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<213> Homo sapiens

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Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
20 25 30

Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
35 40 45

Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
50 55 60

Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65 70 75 80

Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
85 90 95

Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
100 105 110

Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
115 120 125

His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
130 135 140

Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145 150 155 160

Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
 165 170 175

Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
 180 185 190

Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
 195 200 205

Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
 210 215 220

Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
 225 230 235 240

Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
 245 250 255

Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
 260 265 270

Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
 275 280 285

Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
 290 295 300

Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
 305 310 315 320

Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
 325 330 335

Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
 340 345 350

Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
 355 360 365

Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
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Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
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Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
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<400> 4
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 20 25 30
 Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
 35 40 45
 Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
 50 55 60
 Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
 65 70 75 80
 Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
 85 90 95
 Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
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 His Asp Cys Ala Asp Gly Lys
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Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly
 35 40 45
 Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val
 50 55 60
 Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr
 65 70 75 80
 Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu
 85 90 95
 Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala
 100 105 110
 Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser
 115 120 125
 Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys
 130 135 140
 Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile
 145 150 155 160
 Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln
 165 170 175
 Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln
 180 185 190
 Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala
 195 200 205
 Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 210 215 220
 Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser
 225 230 235 240
 Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg
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 Gly Leu Ala Leu
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<212> PRT

<213> Homo sapiens

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20 25 30

Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
35 40 45

Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
50 55 60

Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65 70 75 80

Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
85 90 95

Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
100 105 110

Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
115 120 125

His Asp Cys Ala Asp Gly Lys Leu Lys Phe Gln Cys Gly Gln Lys Thr
130 135 140

Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu
145 150 155 160

Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser
165 170 175

Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile
180 185 190

Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile
195 200 205

Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met
210 215 220

Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp
225 230 235 240

Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys
245 250 255

Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu
260 265 270

Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr
275 280 285

Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu
290 295 300

Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro
305 310 315 320

His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp
325 330 335

Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu
340 345 350

Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp
355 360 365

Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val
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Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly
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Leu Ala Leu

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275

280

285

Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val
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Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly
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Leu Ala Leu

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Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
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Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
 20 25 30

Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
 35 40 45

Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
 50 55 60

Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
 65 70 75 80

Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
 85 90 95

Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
 100 105 110

Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
 115 120 125

His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu
 130 135 140

<210> 9

<211> 96

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<213> Homo sapiens

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Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser
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Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val
20 25 30

Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly
35 40 45

Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro
50 55 60

Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met
65 70 75 80

Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu
85 90 95

<210> 10

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<212> DNA

<213> Homo sapiens

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agatctgatg ctcttcagct gggcctgggg aaacataatt actgcaggaa cccagacaac 180
cggaggcgac cctgggtgcta tgtgcagggtg ggcctaaagc cgcttgtcca agagtgcattg 240
gtgcatgact gcgcagatgg aaaa 264

<210> 11

<211> 141

<212> DNA

<213> Homo sapiens

<400> 11

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cactgtgaaa tagataagtc a 141

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 cactgtgaaa tagataagtc aaaaacctgc tatgagggga atggtcactt ttaccgagga 180
 aaggccagca ctgacaccat gggccggccc tgccctgccct ggaactctgc cactgtcctt 240
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 tactgcagga acccagacaa ccggaggcga ccctggtgct atgtgcaggt gggcctaaag 360
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 cactgtgaaa tagataagtc aaaaacctgc tatgagggga atggtcactt ttaccgagga 180
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 cagcaaacgt accatgcccc cagatctgat gctcttcagc tgggcctggg gaaacataat 300
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<212> DNA

<213> Homo sapiens

<400> 14

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atctacagga ggcaccgggg gggctctgtc acctacgtgt gtggaggcag cctcatcagc 180
ccttgctggg tgatcagcgc cacacactgc ttcattgatt acccaaagaa ggaggactac 240
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tggggccgtg gatgtgccct gaaggacaag ccaggcgctc acacgagagt ctcacacttc 780
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<212> DNA

<213> Homo sapiens

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 actttgactg gaattgtgag ctggggccgt ggatgtgccc tgaaggacaa gccaggcgtc 900
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 <211> 429
 <212> DNA
 <213> Homo sapiens

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 cactgtgaaa tagataagtc aaaaacctgc tatgagggga atggctcactt ttaccgagga 180
 aaggccagca ctgacaccat gggccggccc tgcctgccct ggaactctgc cactgtcctt 240
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 tactgcagga acccagacaa ccggaggcga ccctggtgct atgtgcaggt gggcctaaag 360
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 ccagaagaa 429

<210> 18
 <211> 288
 <212> DNA
 <213> Homo sapiens

<400> 18

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cggaggcgac cctgggtgcta tgtgcaggtg ggcctaaagc cgcttgtcca agagtgcatt 240
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